

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 / Search time 43.7273 Seconds
(without alignment)
1225.145 Million cell updates/sec

Title: US-09-988-971-2_COPY_2_261

Perfect score: 1346
Sequence: 1 GSELRKRLSPSPSLSSVQ.....RESLSFYISLNDVAVSDDA 260

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_rodent:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1346	100.0	261	4 Q9H6Q3	Q9H6Q3 homo sapien
2	1040	77.3	197	4 Q9H135	Q9H135 homo sapien
3	1027	76.3	259	11 Q8V142	Q8V142 mus musculu
4	1018	75.6	259	11 Q8R410	Q8R410 mus musculu
5	933.5	69.4	210	4 Q8WY18	Q8WY18 homo sapien
6	751.5	55.8	179	11 Q8D129	Q8D129 mus musculu
7	495.5	36.8	280	11 Q8QZK8	Q8QZK8 mus musculu
8	495.5	36.8	281	11 Q60898	Q60898 mus musculu
9	485.5	36.1	276	4 Q13339	Q13339 homo sapien
10	370.5	27.5	502	13 Q9DDK6	Q9DDK6 salmo salar
11	364.5	27.1	488	13 Q13064	Q13064 xenopus lae
12	362.5	26.9	161	4 Q9HB17	Q9HB17 homo sapien
13	356.5	26.5	505	4 Q961N1	Q961N1 homo sapien
14	344	25.6	509	6 Q95M32	Q95M32 hylobates s
15	342.5	25.4	509	11 Q91X65	Q91X65 mus musculu
16	336	25.0	517	5 Q9V9J3	Q9V9J3 drosophila

17	332	24.7	509	6 Q95KR7	Q95KR7 salmtr sci
18	319.5	22.7	537	11 Q62844	Q62844 rattus norv
19	315	23.4	496	13 Q93411	Q93411 xenopus lae
20	313.5	23.3	541	11 Q99PW1	Q99PW1 rattus norv
21	313	23.3	812	15 Q85466	Q85466 y73 sarcoma
22	311	23.1	517	11 Q63206	Q63206 rattus norv
23	310	23.0	534	4 Q16248	Q16248 homo sapien
24	310	23.0	534	6 Q95M31	Q95M31 hylobates s
25	309	23.0	527	5 Q9Y121	Q9Y121 ephydaria f
26	307.5	22.8	517	5 Q77050	Q77050 anthracidi
27	301	22.4	63	4 Q96Q14	Q96Q14 homo sapien
28	292.5	21.7	587	5 Q64817	Q64817 avian sarco
29	289	21.5	511	5 Q8WQMS	Q8WQMS strongyloce
30	288.5	21.4	503	5 Q8WSU5	Q8WSU5 ephydaria f
31	286	21.2	502	13 Q8QC39	Q8QC39 fuqu rubrip
32	284.5	21.1	523	15 Q85477	Q85477 rous sarcom
33	284.5	21.1	526	15 Q64994	Q64994 rous sarcom
34	281.5	20.9	528	15 Q93080	Q93080 rous sarcom
35	280	20.8	535	15 Q92957	Q92957 rous sarcom
36	279.5	20.8	526	15 Q64993	Q64993 rous sarcom
37	279	20.7	546	15 Q86363	Q86363 rous sarcom
38	277.5	20.6	526	15 Q92806	Q92806 rous sarcom
39	277.5	20.6	542	11 Q9J110	Q9J110 rattus norv
40	277	20.6	545	15 Q86362	Q86362 rous sarcom
41	274.5	20.4	495	5 Q8WSU4	Q8WSU4 ephydaria f
42	274	20.4	504	5 Q8WSU2	Q8WSU2 ephydaria f
43	273.5	20.3	526	15 Q07461	Q07461 rous sarcom
44	272.5	20.2	526	15 Q60567	Q60567 rous sarcom
45	264.5	19.7	507	5 Q45539	Q45539 caenorhabdi

ALIGNMENTS

RESULT 1

Q9H6Q3 PRELIMINARY; PRT; 261 AA.

AC Q9H6Q3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CDNA: FL21992 fls, clone HEP06554 (Src-like adapter protein-2)
DE (Modulator of antigen receptor signaling MARS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kambata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani T., Nakamura Y., Isogai T., Sugano S.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE:2155259; PubMed:11695592;
RA Holland C.V., Liao X.C., Wendenhall M.K., Zhou X., Pardo J., Chu P.,
RA Spencer C., Fu A.C., Sheng N., Yu P., Pail E., Nagin A., Shen M.,
RA Yu S., Chan E., Wu X., Li C., Woloszewski M., Aversa G.,
RA Kolbinger F., Bennett M.K., Molineaux S., Luo Y., Payan D.G.,
RA Mancoff H.S.V., Wu J.,
RT "Functional cloning of src-like adapter protein-2 (SLAP-2), a novel
RT inhibitor of antigen receptor signaling."
RL J. Exp. Med. 194:1263-1276(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Loreto M.P., McGlade C.J.,
RT "Modulator of Antigen Receptor Signaling (MARS)."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AK025645; BAB15201.1; -.

DR EMBL; AF326353; AAL29204.1; -
 DR EMBL; AF290985; AAL38197.1; -
 DR HSSP; P06239; LTK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SMO0252; SH2; 1.
 DR SMART; SMO0326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM SH3 domain; Receptor
 SQ SEQUENCE 261 AA; 28585 MW; 858AF03451672B3D CRC64;

Query Match 100.0%; Score 1346; DB 4; Length 261;
 Best Local Similarity 100.0%; Pred. No. 4,9e-115;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSLPRRRKSLSPSSSSVVOGQGVPTMEARSKATVALGSPAGPAELSLRLGEPLTI 60
 DB 2 GSLPRRRKSLSPSSSSVVOGQGVPTMEARSKATVALGSPAGPAELSLRLGEPLTI 61
 QY 61 VSEDDGMMTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPGNPGGAFILIR 120
 DB 62 VSEDDGMMTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPGNPGGAFILIR 121
 QY 121 ESQTRRGYSISVRLSRPASMRIHRYHICLDNGMLYISPLTSPSLQALVDHYSELAD 180
 DB 122 ESQTRRGYSISVRLSRPASMRIHRYHICLDNGMLYISPLTSPSLQALVDHYSELAD 181
 QY 181 DICLLKEPCVLQAGPLPGKDIPLVTVQRTPLMWKELDSLLFSEATGEESSLISEGL 240
 DB 182 DICLLKEPCVLQAGPLPGKDIPLVTVQRTPLMWKELDSLLFSEATGEESSLISEGL 241
 QY 241 RESLSFYISLNDENVSLDDA 260
 DB 242 RESLSFYISLNDENVSLDDA 261

RESULT 2
 Q9H135 PRELIMINARY; PRT; 197 AA.

AC Q9H135; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE D0977B1.1 (Novel protein tyrosine kinase with Src homology domain 2 (SH2) domain) (Fragment).
 GN D0977B1.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1] TaxId=9606;
 RP SEQUENCE FROM N.A.
 RA Lloyd D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050318; CAB75365.1; -
 DR HSSP; P06239; LTK.
 DR InterPro; IPR000980; SH2.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SMO0252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 KM Kinase.
 FT NON_TER
 SQ SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;

Query Match 77.3%; Score 1040; DB 4; Length 197;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 64 DGDMMTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPGNPGGAFILIR 123
 DB 1 DGDMMTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPGNPGGAFILIR 120
 QY 124 TRRGYSISVRLSRPASMRIHRYHICLDNGMLYISPLTSPSLQALVDHYSELADIC 183
 DB 61 TRRGYSISVRLSRPASMRIHRYHICLDNGMLYISPLTSPSLQALVDHYSELADIC 120
 QY 184 CLKEPCVLQAGPLPGKDIPLVTVQRTPLMWKELDSLLFSEATGEESSLISEGLRES 243
 DB 121 CLKEPCVLQAGPLPGKDIPLVTVQRTPLMWKELDSLLFSEATGEESSLISEGLRES 180
 QY 244 LSFTYISLNDENVSLDDA 260
 DB 181 LSFTYISLNDENVSLDDA 197

RESULT 3

OBV142 PRELIMINARY; PRT; 259 AA.
 ID OBV142; 01-MAR-2002 (Tremblrel. 20, Created)
 AC OBV142; 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 21, Last annotation update)
 DE Modulator of antigen receptor signaling MARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loreto M.P., McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS).";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF287467; AAL38196.1; -
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SMO0252; SH2; 1.
 DR SMART; SMO0326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM Receptor.
 SQ SEQUENCE 259 AA; 28476 MW; 8270F17C03F50A3 CRC64;

Query Match 76.3%; Score 1027; DB 11; Length 259;
 Best Local Similarity 79.7%; Pred. No. 7.4e-86;
 Matches 208; Conservative 16; Mismatches 33; Indels 4; Gaps 3;

QY 1 GSLPRRRKSLSPSSSSVVOGQGVPTMEARSKATVALGSPAGPAELSLRLGEPLTI 60
 DB 2 GSLPRRRKSLSPSSSSVVOGQGVPTMEARSKATVALGSPAGPAELSLRLGEPLTI 60
 QY 61 VSEDDGMMTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPGNPGGAFILIR 120
 DB 61 VSEDDGMMTVLSEVSGREYNIPSVHAKVSHGWLVEGLSREKAEELLPGNPGGAFILIR 120
 QY 121 ESQTRRGYSISVRLSRPASMRIHRYHICLDNGMLYISPLTSPSLQALVDHYSELAD 180
 DB 121 ESQTRRGYSISVRLSRPASMRIHRYHICLDNGMLYISPLTSPSLQALVDHYSELAD 180
 QY 181 CLKEPCVLQAGPLPGKDIPLVTVQRTPLMWKELDSLLFSEATGEESSLISEGL 239
 DB 181 CLKEPCVLQAGPLPGKDIPLVTVQRTPLMWKELDSLLFSEATGEESSLISEGL 240
 QY 240 LRESLSFYISLNDENVSLDDA 260

DB 241.LRESLSYS1SLAED--PLDDA 259

RESULT 4

ID Q8R410

PRELIMINARY; PRT; 259 AA.

AC Q8R410;

01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS Strc-like adapter protein-2.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Pandey A., Ibarrola N., Kratchmarova I., Fernandez M.,

RA Constantinescu S., Ohara O., Sawadiksol S., Lodish H.F., Mann M.;

RT "A novel Src homology 2 domain-containing molecule, Src-like Adapter

RT Protein-2 (SLAP-2), which negatively regulates T cell receptor

RT signaling."

RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Ibarrola N., Mann M., Pandey A.;

RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF34990; AAL86403.1; -

SQ SEQUENCE 259 AA; 28516 MW; 138868244152B34 CRC64;

Query Match 75.6%; Score 1018; DB 11; Length 259;
Best Local Similarity 79.3%; Pred. No. 4.9e-85;
Matches 207; Conservative 16; Mismatches 34; Indels 4; Gaps 3;

QY 1 GSLPSRRKSLPSPLSSVQGGPYTMEERSKATVAVALGSPAGPAPLSLRGEPIT 60
DB 2 GSLSRRKSLPSPLSSVQGGPYTMEERSKATVAVALGSPAGPAPLSLRGEPIT 60

QY 61 VSEDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEILLPGNPGCAFIR 120
DB 61 ISEBDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEILLPGNPGCAFIR 120

QY 121 ESOTRRGYSYLSVRLSPASWDRIHRYHICLDNGWLYISPRITFPSIQALVDHYS 180
DB 121 ESOTRRGYSYLSVRLSPASWDRIHRYHICLDNGWLYISPRITFPSIQALVDHYS 180

QY 181 DICCLKEPCVLORAGPPLPGDIPLPVTYQRTPLNWKELDSSLIFSEA-ATGESILSEG 239
DB 181 GICCPLEPCVLQKGPPLPGDTPPTVPTVTSLLMVKLLDSSLIFLEAPASGEAATLSEG 240

QY 240 LRESLSYS1SLAED--PLDDA 260
DB 241 LRESLSYS1SLAED--PLDDA 259

RESULT 5
Q8WY18 PRELIMINARY; PRT; 210 AA.

ID Q8WY18

PRELIMINARY; PRT; 210 AA.

AC Q8WY18;

01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS Modulator of antigen receptor signaling, putative splice isoform

DE MARS-V.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Loreto M.P., McGlade C.J.;

RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice

RT variant.";

RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF290986; AAL38198.1; -

DR InterPro; IPR000980; SH2.

DR InterPro; IPR00452; SH3.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR ProDom; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS00001; SH2; 1.

DR PROSITE; PS00002; SH3; 1.

KW Receptor.

SQ SEQUENCE 210 AA; 23103 MW; BBD62208E53A472E CRC64;

Query Match 69.4%; Score 933.5; DB 4; Length 210;
Best Local Similarity 89.3%; Pred. No. 2e-77;
Matches 184; Conservative 3; Mismatches 12; Indels 7; Gaps 1;

QY 1 GSLPSRRKSLPSPLSSVQGGPYTMEERSKATVAVALGSPAGPAPLSLRGEPIT 60
DB 2 GSLSRRKSLPSPLSSVQGGPYTMEERSKATVAVALGSPAGPAPLSLRGEPIT 61

QY 61 VSEDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEILLPGNPGCAFIR 120
DB 62 VSEDGDMWTVLSEVSGREYNIPSVHAKVSHGLYEGSRKAEILLPGNPGCAFIR 121

QY 121 ESOTRRGYSYLSVRLSPASWDRIHRYHICLDNGWLYISPRITFPSIQALVDHYS 177
DB 122 ESOTRRGYSYLSVRLSPASWDRIHRYHICLDNGWLYISPRITFPSIQALVDHYS 181

QY 178 ----LADDICCLKEPCVLORAGPPL 199
DB 182 APWGGTPTCCACEDTTQLRAGQLP 207

RESULT 6
Q8D129 PRELIMINARY; PRT; 179 AA.

ID Q8D129

PRELIMINARY; PRT; 179 AA.

AC Q8D129;

01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

OS A93000922IRIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=RETINA;

RA MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,

RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baran G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,

RA Guetlich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whiteaker C., Wilming L.,

RA Watanabe-Borja A., Yoshida K., Hasegawa Y., Kawai H., Kohno S.,

RA Hayashizaki Y.;

0 8525555---L5555GGGGPVM1AEKSKAIAIAVALGSF-PAGGPARLSRLTGEPLTIVSED 64
 || || |||| | ||| :| : ||| :||:|
 || || |||| | ||| :| : ||| :||:|

Best Local Similarity 43.9%; Pred. No. 3.5e-37;
Matches 116; Conservative 38; Mismatches 81; Indels 29; Gaps 7;
8 KSI:PPPS-----LSSVVGCGDPYTMFAEPKSKATVAIVLCSFPDAGCAPLSTLPIGRPIITTVSEFN 64

8 KSLPSPS---LSSSVOGGPMTEAERSKATAVALGSPAGGPAEISLRIGEPITVISED 64
Best Local Similarity 43.9%; Pred. No. 3.5e-37;
Matches 116; Conservative 38; Mismatches 81; Indels 29; Gaps 7;

```

Db      6, KSTSPSPERPLSS-----EGLESDPLAV-LTDYPSDIPSPPIFRGKGLRVISDE 55
Qy      65 GDMWTVLSEVSGREYNIPSVHAKVSHGMLYEGLSREAEELLILPGNPGAFILRSQT 124
Db      56 GGMWKAISLSTGRESYIPGICVAVYHGMVFEGLGRDAEBLLQLPDTIGCFMIRSET 115
Qy      125 RRGYSLSVRLSRPASWDRIRHYRICHLDNGMLYISPLTFPSLOALVDHYSELDADIC 184
Db      116 KKGFSLSVSR-----HRQVNHYRIFRLPNMNYISPLTFQCLDVLNHYSEVADGLCC 169
Qy      185 LKAEPCVLR-----AGPLPGKDIPLPTVQRTPLNWKELDSLLFSEATG---EESL 235
Db      170 VLTPLAQNIPAPTSHPSPCTGSPVTLRQKTPDMKRVSRLOEGSGEAEPLRVVSESL 229
Qy      236 LSEGLRESLSFYISL-NDEAVSLD 258
Db      230 FSYGLRESIASYLSLTGDDSSSD 253

RESULT 9
ID      Q13239      PRELIMINARY;      PRT;      276 AA.
AC      Q13239;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE      Putative SRC-like adapter protein (SLAP) (SRC-like-adapter).
GN      SLAP.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96423054; PubMed=8825655;
RA      Angrist M., Wells D.E., Chakravarti A., Pandey A.;
RT      "Chromosomal localization of the mouse Src-like adapter protein (Slap)
RL      gene and its putative human homolog SLA.";
RN      Genomics 30:623-625(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BRIN;
RA      Meijerink P.H.S., Zorn G., Bikker H., Bolhuis P.A., Baas F.;
RL      Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Ohtsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
RL      Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RA      Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
RA      Jonge, R., Schilhabel M., Wen G., Menzel U., Detle M., Baungart C.,
RA      Rosenthal A.;
RL      Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BONE MARROW;
RA      Strausberg R.;
RL      Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC      -i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR      EMBL; U30473; AAC50357.1; -
DR      EMBL; U44403; AAC27662.1; -
DR      EMBL; D89077; BA13758.1; -
DR      EMBL; AF305872; AAG17933.1; -
DR      EMBL; BC007042; AAH07042.1; -
DR      HSSP; P08631; 3KCK.
DR      InterPro; IPR000980; SH2.
DR      InterPro; IPR001452; SH3.
DR      Pfam; PF00017; SH2; 1.
DR      Pfam; PF00018; SH3; 1.
DR      PRINTS; PR00401; SH2DOMAIN.
DR      ProDom; PD000093; SH2; 1.

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DR      SMART; SM00252; SH2; 1.
DR      SMART; SM00326; SH3; 1.
DR      PROSITE; PS50001; SH2; 1.
DR      PROSITE; PS50002; SH3; 1.
DR      SH3 domain.
SQ      SEQUENCE 276 AA; 31156 MW; 80FC7D7B2E3A378 CRC64;

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Query Match      36.1%; Score 485.5; DB 4; Length 276;
Best Local Similarity 40.7%; Preq. No. 2,8e-36;
Matches 103; Conservative 43; Mismatches 84; Indels 23; Gaps 4;

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Qy      8 KSLPSPSSSSVOCGFVTMEARSKATAVAGLSFPAGCPAEISRLGEPLTIVSEDCGW 67
Db      6 KSTPAPA-----ERLPPMPEGDSDPLAVLSQYPEPDISPIFRGKGLRVISDEGCGW 58
Qy      68 WTVLSEVSGREYNIPSVHAKVSHGMLYEGLSREAEELLILPGNPGAFILRSQTRG 127
Db      59 WKAIISLSTGRESYIPGICVAVYHGMVFEGLGRDAEBLLQLPDTIGCFMIRSETKKG 118
Qy      128 SYSLSVRLSRPASWDRIRHYRICHLDNGMLYISPLTFPSLOALVDHYSELDADICCLAK 187
Db      119 FYSLSVR-----HRQVNHYRIFRLPNMNYISPLTFQCLDVLNHYSEVADGLCCVLT 172
Qy      188 EPCVLRAGPLPGKDIPLPTVQRTPLNWKELDSLLFSEATG-----EESLSSEG 240
Db      173 TPCLTSTAPAVASSPVTLRQKTPDMKRVSR--LQDEPGENPLGVDSLSFYGL 229
Qy      241 RESLSFYISLND 253
Db      230 RESIASYLSLTSE 242

RESULT 10
ID      Q9DDK6      PRELIMINARY;      PRT;      502 AA.
AC      Q9DDK6;
DT      01-MAR-2001 (TREMBlrel. 16, Created)
DT      01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Src-family tyrosine kinase SKC.
OS      Salmo salar (Atlantic salmon).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protactinopterygii; Salmoniformes; Salmonidae; Salmo.
OX      NCBI_Taxid=8030;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Hordvik I., Male R.;
RT      "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine
RL      kinase.";
RN      Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC      -i- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR      EMBL; AF321110; AAC38611.1; -
DR      HSSP; P08631; 1AD5.
DR      InterPro; IPR000719; Euk_pkinase.
DR      InterPro; IPR002290; Src_thr_pkinase.
DR      InterPro; IPR000980; SH2.
DR      InterPro; IPR001452; SH3.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00069; pkinase; 1.
DR      Pfam; PF00017; SH2; 1.
DR      Pfam; PF00018; SH3; 1.
DR      PRINTS; PR00401; SH2DOMAIN.
DR      PRINTS; PR00452; SH3DOMAIN.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD000001; Euk_pkinase.
DR      ProDom; PD000066; SH3; 1.
DR      ProDom; PD000093; SH2; 1.
DR      SMART; SM00252; SH2; 1.
DR      SMART; SM00326; SH3; 1.
DR      SMART; SM00220; S_TKc; 1.
DR      SMART; SM00219; TYTKc; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM ATP-binding; Kinase; SH3 domain; Transferase.
 SQ SEQUENCE 502 AA; 5660 MW; 82DF0D677AA99980 CRC64;

Query Match 27.5%; Score 370.5; DB 13; Length 502;
 Best Local Similarity 42.4%; Pred. No. 2.1e-25;
 Matches 81; Conservative 29; Mismatches 66; Indels 15; Gaps 3;

QY 14 SLSSSVGQGPVTMEARSKATAVALGSPAGPAELSLRLGEPITVSDGDMVTVSE 73
 DB 45 STGSPESDGE-----ESTALALDYEGINEGDLGPKKDKLTLQSGEMRAQSI 96
 QY 74 VSGREYNIPSVHAKVS---HGMLYEGLSREKAEELLPLGNPGCAFILRESQTRRGYS 130
 DB 97 STGDEGFIPIPSNYVALIDSLTEEMFPGVSRDAERQLLASGNKGSFMIDSEPTTKGSYS 156
 QY 131 LSVRLSPASWDRIHRYRHICLDNGMLYISPLTPPSLQALVDHYSELAADICLKEPC 190
 DB 157 LSVRSDSDSGDVIYKHKIRTLNDNGFIISPRITFTTLOELVSHYKKLGDLQALTPSC 216
 QY 191 VLQRAGLPGK 201
 DB 217 L-----SPKPK 223

RESULT 11
 ID 013064 PRELIMINARY; PRT; 488 AA.
 AC 013064;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Lyn protein tyrosine kinase.
 GN LYN.
 OS Xenopus laevis (African clawed frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
 OC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN (1) --
 RP SEQUENCE FROM N.A.
 RA Fukami Y., Funabiki K., Sato K.;
 RT "Nucleotide sequence of Xenopus Lyn protein tyrosine kinase.";

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AB003358; BAA20078.1; -.
 DR HSSP; P08631; IAD5.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; I.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SMO0252; SH2; 1.
 DR SMART; SMO0326; SH3; 1.
 DR SMART; SMO0219; TYRKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 488 AA; 55794 MW; B7E70668B6A92B2 CRC64;

Query Match 27.1%; Score 364.5; DB 13; Length 488;
 Best Local Similarity 40.1%; Pred. No. 7.1e-25;
 Matches 81; Conservative 33; Mismatches 69; Indels 19; Gaps 4;

QY 5 SRRKS-LPSPSSSSVGQGPVTMEARSKATAVALGSPAGPAELSLRLGEPITVSE 63
 DB 22 SRTSLIPQCKIIOIEQNI-----VIALPYGHHEDLSFKKGEKLVLEE 71
 QY 64 GDMVTVSEVSGREYNIPSVHAKV---SHGMLYEGLSREKAEELLPLGNPGCAFIL 119
 DB 72 HGEWKKAKSLSTKKEGFIPIPSNYAVNTLETMEFMDLTRKDAERQLLAPGNNGAFIL 131
 QY 120 RESQTRRGYSVLSLSPASWDRIHRYRHICLDNGMLYISPLTPPSLQALVDHYSELA 179
 DB 132 RESSTSGSYSLSIDCPQCGDVIYKHKIRTLNDNGGVIISPRITFTSINEMIQYKQA 191
 QY 180 DDIICLKEPCVLQRAGLPGK 201
 DB 192 DGLCRKLDKPCF-----SPKPK 209

RESULT 12
 ID 09HB17 PRELIMINARY; PRT; 161 AA.
 AC 09HB17;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Src-like adapter protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN (1) --
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonge, Rd., Schellabel M.B., Menzel U., Dette M.D., Baumgart C.,
 RA Jahn N., Rosenthal A.;
 RT "Chromosome 8 genomic sequence";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN (2) --
 RP SEQUENCE FROM N.A.
 RA Genome Sequencing Center Jena;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF235100; AAG29878.1; -.
 DR HSSP; P08631; 3HCK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SMO0252; SH2; 1.
 DR SMART; SMO0326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM SH3 domain.
 KW NON TER 161
 FT NON TER 161
 SQ SEQUENCE 161 AA; 18493 MW; FC285466804E5B20 CRC64;

Query Match 26.9%; Score 362.5; DB 4; Length 161;
 Best Local Similarity 44.4%; Pred. No. 2.4e-25;
 Matches 75; Conservative 27; Mismatches 54; Indels 13; Gaps 2;

QY 8 KSLPSSLSSVGQGPVTMEARSKATAVALGSPAGPAELSLRLGEPITVSDGDW 67
 DB 6 KSTPAFA-----ERPLPNEGGLSDFLAVSDYPSDIPPIFRKGEKLVISDEGW 58
 QY 68 WTVLSEVSGREYNIPSVHAKVSHGMLYEGLSREKAEELLPLGNPGCAFILRESQTRRG 127
 DB 59 WKALSLSTGESEITPGLCAKRVYHGMFLRGLGRDAEELLQPLPTKVGSMIRSETKKG 118

QY 126 SYSIVRLSRPASWDRIKRYRICHLDNGWLYISPRITPSIQALVDHYS 176
 DB 119 FYSLSVR-----HROVKHYRIFPLPNWYISPRITPSIQALVDHYS 161

RESULT 13

096IN1 PRELIMINARY; PRT; 505 AA.

AC 096IN1, 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Unknown (protein for MGC:16168).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 ON NCBI_TaxID=9606;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strauberg R.;
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC007371; AA07371.1; -;
 DR InterPro; IPR000719; Euk_Pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProSite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR ProSite; PS00011; PROTEIN_KINASE_DOM; 1.
 DR ProSite; PS50001; SH2; 1.
 DR ProSite; PS50002; SH3; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 505 AA; 57706 MW; B5F73BEF839176 CRC64;

Query Match 26.5%; Score 356.5; DB 4; Length 505;
 Best Local Similarity 44.2%; Pred. No. 4e-24;
 Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;

QY 24 PVTMEARSKATAVALGSPAGPAELISRLGEPLTIVSEDDGMWTVLSEVSGREYNIPS 83
 DB 51 PRDEHLEDKGFVALYDYTAMNDRDQMLKGBKLQVKGKGTGDMWTLARSLVTRGGYVPS 110
 QY 84 VHVAKVS---HGMLYEGLSREKAEELLLPGNPGCAFLLRESQTRGSGYSLSVR 139
 DB 111 NPYARVSLSEMERWPFPSQGRKAEKROLAPITKAGSFLRESSTNGAFSLSVK-DVTT 169
 QY 140 SMDRIHYRIHCLDNGWLYISPRITPSIQALVDHYSLEADICLLKEPCV 191
 DB 170 QGELIKHYKIRCLDEGGYVISPRTTSPSIQALVQHSKKGDLGCLORLTJPCV 221

RESULT 14

095M32 PRELIMINARY; PRT; 509 AA.

AC 095M32, 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DE Lck protein.
 OS Lck.
 OS Hylobates sp. (gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 ON NCBI_TaxID=9581;
 RX (1)
 RP SEQUENCE FROM N.A.
 RA Picard C.;

RL Thesis (2001). Department of Experimental Oncology Laboratory, U.
 DR EMBL; AJ320182; CAC44027.1; -;
 DR InterPro; IPR000719; Euk_Pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProSite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR ProSite; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ProSite; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR ProSite; PS50001; SH2; 1.
 DR ProSite; PS50002; SH3; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 509 AA; 57946 MW; F1BF5C237C8DB7E CRC64;

Query Match 25.6%; Score 344; DB 6; Length 509;
 Best Local Similarity 41.1%; Pred. No. 5.6e-23;
 Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2;

QY 25 VTMERASRAT-----AVLGSFPAGPAELISRLGEPLTIVSEDDGMWTVLSEVSGRE 78
 DB 49 VTGEGSNPPASPLQDNLVIALHSYEPSSHDDGEGEKKEQRILESGEWMVAQSLLTGGOE 108
 QY 79 YNIPSVHAKVS---HGMLYEGLSREKAEELLLPGNPGCAFLLRESQTRGSGYSLSVR 134
 DB 109 GFIPFVFAKANSLEPEWPFKXLSKQAEKQLAPNTGHTGSLRESSTNGAFSLSVK 168
 QY 135 LSRPASWDRIKRYRICHLDNGWLYISPRITPSIQALVDHYSLEADICLLKEPCV 194
 DB 169 DFDQNGEVVAKHYKIRCLDNGGYVISPRTTSPSIQALVQHSKKGDLGCLORLTJPCV 228

RESULT 15

091X65 PRELIMINARY; PRT; 509 AA.

AC 091X65, 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Similar to lymphocyte-specific protein tyrosine kinase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary Gland;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC011474; AAH11474.1; -;
 DR MGD; MG1:96756; Lck.
 DR InterPro; IPR000719; Euk_Pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; Tyr_Pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProSite; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR ProSite; PS50011; PROTEIN_KINASE_DOM; 1.
 DR ProSite; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR ProSite; PS50001; SH2; 1.
 DR ProSite; PS50002; SH3; 1.
 KW ATP-binding; Kinase; Transferase.

SEQ SEQUENCE 509 AA; 57942 MW; 3513102F49A7FDOB CRC64;

Query Match 25.4%; Score 342.5; DB 11; Length 509;

Best Local Similarity 39.6%; Pred. No. 7,7e-23;

Matches 78; Conservative 28; Mismatches 84; Indels 7; Gaps 2;

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OY 2 SLPSRRKSLPPSLSSVQGGQGVTEAEERSKATAVAGSPFAGGPAELSLRIGEPULTV 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 35 SLPIRNGSEVRDPL--VTVESGLPPASPLQDNLVIALHSEYSPSHDGLGFEKGEQLRL 91
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 62 SEDGMWTVLSEVSGREYNIPSVHAKVS---HGWLYEGLSREKAEELLLPGNPGAF 117
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 92 EDSGEWMAQSLTGTGQSGFTFNFVAKANSLEPEPWFKNLSRKDAERQLAPGNTHSGF 151
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 118 LIREQTRRGSYSLVRLSRPASMDRIHRYRIHCLDNGMLYISPRLPSPLOALVDHISE 177
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 152 LIRESESTAGSFSLSVDPDONQGEVVGKIRLNDGGFYISPRITPPGLHDLVRYHTN 211
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 178 LADICCLKEPCVLQR 194
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 212 ASDGLCTKISRRCQCTOK 228
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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Search completed: March 24, 2003, 15:50:34
Job time : 45.7273 secs